



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 149432

TO: Nita M Minnifield  
Location: rem/3c01/3c18  
Art Unit: 1645  
Friday, April 01, 2005

Case Serial Number: 09/914454

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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OM nucleic - nucleic search, using sw model

March 31, 2005, 17:42:45 ; Search time 125 Seconds

(without alignments)  
395.473 Million cell updates/sec

File: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hcc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	498	9	CL978668
2	20	100.0	2799	9	CL978665
3	18.4	92.0	886	9	CC709713
4	17.4	87.0	698	7	CN928980
5	17.4	87.0	1062	9	CL970339
6	17.4	85.0	1088	6	CD505499
7	17.4	85.0	2805	7	CL965273
8	16.8	84.0	287	2	BF713668
9	16.8	84.0	389	9	CG260054
10	16.8	84.0	464	1	AA117941
11	16.8	84.0	497	9	CL119555
12	16.8	84.0	516	2	BF156008
13	16.8	84.0	546	2	AM065908
14	16.8	84.0	557	6	CA158051
15	16.8	84.0	614	6	CA113844
16	16.8	84.0	646	6	CA109803
17	16.8	84.0	663	6	CA153904
18	16.8	84.0	668	6	CA264770
19	16.8	84.0	683	6	CA182313
20	16.8	84.0	715	5	BU253412
21	16.8	84.0	729	7	CV181077
22	16.8	84.0	758	8	CC110844
23	16.8	84.0	794	9	CG334934
24	16.8	84.0	797	9	CNS02N06

C	25	16.8	84.0	814	5	BU205165
C	26	16.8	84.0	821	9	CNS03064
C	27	16.8	84.0	842	9	CG319646
C	28	16.8	84.0	864	9	CG318330
C	29	16.8	84.0	908	6	CD791886
C	30	16.8	84.0	915	5	CG318342
C	31	16.8	84.0	958	5	BO882047
C	32	16.8	84.0	992	9	CNS04004
C	33	16.8	84.0	994	9	CNS0421L
C	34	16.8	84.0	1867	3	CR696760
C	35	16.4	82.0	179	4	BM598254
C	36	16.4	82.0	318	8	AZ578302
C	37	16.4	82.0	392	6	BY630307
C	38	16.4	82.0	398	4	BI033356
C	39	16.4	82.0	553	2	BB767360
C	40	16.4	82.0	596	4	BM592203
C	41	16.4	82.0	643	2	BE647310
C	42	16.4	82.0	648	2	BB529260
C	43	16.4	82.0	665	2	BB183341
C	44	16.4	82.0	680	1	AL694689
C	45	16.4	82.0	695	7	CF531954

## ALIGNMENTS

RESULT 1  
LOCUS CL978668/c 498 bp DNA linear GSS 21-SEP-2004  
DEFINITION OeIFCC032298 Oryza sativa (indica cultivar-group) genomic survey sequence.  
ACCESSION CL978668  
VERSION CL978668.1 GI:52411839  
KEYWORDS  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphorbiaceae; Oryzaeae; Oryza.

## REFERENCE

1 (bases 1 to 498)  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.  
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
Unpublished (2004)

## JOURNAL

COMMENT  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.

## FEATURES

source  
Location/Qualifiers  
1..498  
/organism="Oryza sativa (indica cultivar-group)"  
/mol type="genomic DNA"  
/db xref="taxon:39946"  
/clone lib="Oryza sativa Expressed Library"  
/note="Oryza sativa exon trapped genomic sequences"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 1 TCCATGACGTTCTGACGTT 20  
DB 83 TCCATGACGTTCTGACGTT 64

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Gen Nucleic - nucleic search, using sw model

Run on: March 31, 2005, 17:00:28 ; Search time 312 Seconds  
(without alignments)  
387.980 Million cell updates/sec

File: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacctctcctgacgtt 20

Scoring table: IDENTITY NTC

Gapop 10.0, Gapext 1.0

Searched: 5607317 seqs, 302624599 residues 11214634

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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4	20	100.0	20	9	US-09-824-468-105
5	20	100.0	20	9	US-09-949-194-1
6	20	100.0	20	9	US-09-917-222-1
7	20	100.0	20	9	US-09-800-266A-86
8	20	100.0	20	9	US-09-800-266A-90
9	20	100.0	20	9	US-09-895-007A-86
10	20	100.0	20	9	US-09-895-007A-90
11	20	100.0	20	9	US-09-920-313-86

12	20	100.0	20	9	US-09-920-313-90	Sequence 90, Appl
13	20	100.0	20	10	US-09-888-326-560	Sequence 560, App
14	20	100.0	20	10	US-09-888-326-561	Sequence 561, App
15	20	100.0	20	10	US-09-888-326-562	Sequence 562, App
16	20	100.0	20	10	US-09-888-326-563	Sequence 563, App
17	20	100.0	20	10	US-09-818-918-10	Sequence 10, Appl
18	20	100.0	20	10	US-09-931-583-47	Sequence 47, Appl
19	20	100.0	20	10	US-09-776-479-69	Sequence 69, Appl
20	20	100.0	20	10	US-09-776-479-137	Sequence 137, App
21	20	100.0	20	10	US-09-776-479-152	Sequence 152, App
22	20	100.0	20	10	US-09-776-479-153	Sequence 153, App
23	20	100.0	20	10	US-09-776-479-223	Sequence 223, App
24	20	100.0	20	10	US-09-776-479-302	Sequence 302, App
25	20	100.0	20	10	US-09-776-479-948	Sequence 948, App
26	20	100.0	20	10	US-09-776-479-949	Sequence 949, App
27	20	100.0	20	10	US-09-776-479-950	Sequence 950, App
28	20	100.0	20	10	US-09-776-479-951	Sequence 951, App
29	20	100.0	20	10	US-09-776-479-952	Sequence 952, App
30	20	100.0	20	10	US-09-776-479-953	Sequence 953, App
31	20	100.0	20	10	US-09-776-479-954	Sequence 954, App
32	20	100.0	20	10	US-09-776-479-955	Sequence 955, App
33	20	100.0	20	10	US-09-776-479-956	Sequence 956, App
34	20	100.0	20	10	US-09-776-479-957	Sequence 957, App
35	20	100.0	20	10	US-09-776-479-958	Sequence 958, App
36	20	100.0	20	10	US-09-776-479-959	Sequence 959, App
37	20	100.0	20	10	US-09-554-987B-83	Sequence 83, Appl
38	20	100.0	20	10	US-09-967-464-1	Sequence 1, Appl
39	20	100.0	20	10	US-09-984-365-42	Sequence 42, Appl
40	20	100.0	20	11	US-09-776-479-969	Sequence 69, Appl
41	20	100.0	20	11	US-09-776-479-137	Sequence 137, App
42	20	100.0	20	11	US-09-776-479-152	Sequence 152, App
43	20	100.0	20	11	US-09-776-479-153	Sequence 153, App
44	20	100.0	20	11	US-09-776-479-223	Sequence 223, App
45	20	100.0	20	11	US-09-776-479-302	Sequence 302, App

## ALIGNMENTS

RESULT 1

US-09-760-506-3

Sequence 3, Application US/09760506

Publication No. US20010034330A1

GENERAL INFORMATION:

APPLICANT: Kemsil, Charlotte

TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of Cpg and

FILE REFERENCE: 8449-153-999

CURRENT FILING DATE: 2002-01-12

PRIOR APPLICATION NUMBER: 60/200,853

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/175,840

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: 60/128,608

PRIOR FILING DATE: 1999-04-08

PRIOR APPLICATION NUMBER: 60/095,913

PRIOR FILING DATE: 1998-08-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Motif

US-09-760-506-3

Query Match 100.0%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 tccatgacctctcctgacgtt 20

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Run on:

March 31, 2005, 16:07:48 ; Search time 95 Seconds  
(without alignments)  
344.479 Million cell updates/sec

Title: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacgttccctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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27: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	US-09-133-774-12	Sequence 12, Appl
2	20	100.0	20	US-09-303-862-12	Sequence 12, Appl
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4	20	100.0	20	US-09-030-701-62	Sequence 62, Appl
5	20	100.0	20	US-09-286-098-100	Sequence 100, App
6	20	100.0	20	US-09-286-098-105	Sequence 105, App
7	20	100.0	20	US-08-960-774-10	Sequence 10, Appl
8	20	100.0	20	US-09-082-649B-51	Sequence 51, Appl
9	20	100.0	20	US-09-082-649B-56	Sequence 56, Appl
10	20	100.0	20	US-09-082-649B-58	Sequence 58, Appl
11	20	100.0	20	US-09-325-193A-90	Sequence 90, Appl
12	20	100.0	20	US-09-191-170-97	Sequence 97, Appl
13	20	100.0	20	US-09-690-921-1	Sequence 1, Appl
14	20	100.0	20	US-09-301-822A-1	Sequence 1, Appl
15	20	100.0	20	US-09-692-170C-42	Sequence 42, Appl
16	20	100.0	20	US-09-337-619-10	Sequence 42, Appl
17	20	100.0	20	US-10-405-231A-42	Sequence 42, Appl
18	20	100.0	20	US-10-238-607-42	Sequence 42, Appl
19	20	100.0	20	US-09-984-365-42	Sequence 42, Appl
20	20	100.0	20	US-09-565-906-1	Sequence 1, Appl
21	20	100.0	20	US-09-257-188A-2	Sequence 2, Appl
22	20	100.0	20	US-09-965-101-51	Sequence 51, Appl
23	20	100.0	20	US-09-965-101-56	Sequence 56, Appl
24	20	100.0	20	US-09-965-101-58	Sequence 58, Appl
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27	20	100.0	20	US-09-082-649B-12	Sequence 12, Appl

28	20	100.0	44	US-09-965-101-12	Sequence 12, Appl
29	20	100.0	44	US-09-965-101-13	Sequence 13, Appl
30	17	85.0	17	US-09-030-701-39	Sequence 39, Appl
31	17	85.0	17	US-09-286-098-70	Sequence 70, Appl
32	17	85.0	17	US-08-960-774-70	Sequence 70, Appl
33	17	85.0	17	US-09-325-193A-60	Sequence 60, Appl
34	17	85.0	17	US-09-191-170-64	Sequence 64, Appl
35	17	85.0	17	US-09-337-619-70	Sequence 70, Appl
36	16.8	84.0	20	US-09-133-774-11	Sequence 11, Appl
37	16.8	84.0	20	US-08-386-063-25	Sequence 25, Appl
38	16.8	84.0	20	US-09-303-862-11	Sequence 11, Appl
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41	16.8	84.0	20	US-08-738-652-44	Sequence 44, Appl
42	16.8	84.0	20	US-08-738-652-54	Sequence 54, Appl
43	16.8	84.0	20	US-09-030-701-42	Sequence 42, Appl
44	16.8	84.0	20	US-09-286-098-24	Sequence 24, Appl
45	16.8	84.0	20	US-09-286-098-24	Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-09-133-774-12  
Sequence 12, Application US/09133774B  
Patent No. 5962636  
GENERAL INFORMATION:  
APPLICANT: Bachmaier, Kurt  
APPLICANT: Hessel, Andrew J.  
APPLICANT: Neu M.D., Nikolaus  
APPLICANT: Penninger, Josef M.  
TITLE OF INVENTION: No. 5962636 Peptides Capable of Modulating Inflammatory Heart  
FILE REFERENCE: A-536  
CURRENT APPLICATION NUMBER: US/09/133, 774B  
CURRENT FILING DATE: 1998-08-12  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Chlamydia trachomatis  
FEATURE:  
OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a  
OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from  
US-09-133-774-12

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 TCCATGACGTTCCCTGACGTT 20

RESULT 2  
US-09-303-862-12  
Sequence 12, Application US/09303862  
Patent No. 6034230  
GENERAL INFORMATION:  
APPLICANT: Bachmaier, Kurt  
APPLICANT: Hessel, Andrew J.  
APPLICANT: Neu M.D., Nikolaus  
APPLICANT: Penninger, Josef M.  
TITLE OF INVENTION: No. 6034230 Peptides Capable of Modulating Inflammatory Heart  
FILE REFERENCE: A-536  
CURRENT APPLICATION NUMBER: US/09/303, 862  
CURRENT FILING DATE: 1999-05-03  
EARLIER APPLICATION NUMBER: 09/133, 774

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Ch. nucleic - nucleic search, using sw model

March 31, 2005, 17:02:04 / Search time 1533 Seconds  
(Without alignments)  
632.162 Million cell updates/sec

Read GATC

US-09-914-454B-1

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Search: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

GenBank: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pac: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_srs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Alt No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR078395
2	20	100.0	20	6	AR140451
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5	20	100.0	20	6	AR154681
6	20	100.0	20	6	BD190417
7	20	100.0	20	6	BD205610
8	20	100.0	20	6	BD205615
9	20	100.0	20	6	BD222610
10	20	100.0	20	6	BD251265
11	20	100.0	20	6	BD261152
12	20	100.0	20	6	BD261157
13	20	100.0	20	6	BD261307
14	20	100.0	20	6	BD261311
15	20	100.0	20	6	BD261560
16	20	100.0	20	6	BD267913
17	20	100.0	20	6	BD270813
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25	20	100.0	20	6	CQ815135	CQ815135 Sequence
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37	20	100.0	20	6	AR432433	AR432433 Sequence
38	20	100.0	20	6	AR528730	AR528730 Sequence
39	20	100.0	20	6	AR532211	AR532211 Sequence
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#### ALIGNMENTS

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LOCUS AR078395 12 from patent US 5962636. linear PAT 31-AUG-2000  
DEFINITION Sequence AR078395  
ACCESSION AR078395  
VERSION AR078395.1 GI:10005141  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bachmaier K., Hessel A., John., Neu N. and Penninger J. Martin.  
TITLE Peptides capable of modulating inflammatory heart disease  
JOURNAL Patent: US 5962636-A 12 Oct-1999;  
FEATURES  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

#### ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TCCATGACGTTCCTGACGTT 20  
Db 1 TCCATGACGTTCCTGACGTT 20

RESULT 2  
LOCUS AR140451 20 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 10 from patent US 6207646.  
ACCESSION AR140451  
VERSION AR140451.1 GI:14482947  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kriegl A.M., Kline J., Klinman D. and Steinberg A.D.  
TITLE Immunostimulatory nucleic acid molecules

GenCore version 5.1.6  
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US-09-914-454b-1

March 31, 2005, 16:54:48 / Search time 255 seconds  
(without alignments)  
464,293 Million cell updates/sec

US-09-914-454b-1  
Reflected score: 20  
Sequence: 1 tccatgacctctcctgacct 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseq19908:\*  
3: Geneseq20008:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 2 AAV60950	AAV60950 Unmethy
2	20	100.0	20 2 AAV47683	AAV47683 Unmethy
3	20	100.0	20 2 AAV27667	AAV27667 Immunos
4	20	100.0	20 2 AAZ41946	AAZ41946 IL-12 sec
5	20	100.0	20 2 AAZ41949	AAZ41949 IL-12 sec
6	20	100.0	20 2 AAX78802	AAZ78802 HPV fusio
7	20	100.0	20 2 AAZ31943	AAZ31943 Cpg adjuv
8	20	100.0	20 2 AAV74237	AAV74237 Cpg-N mot
9	20	100.0	20 2 AAV74244	AAV74244 Cpg-N mot
10	20	100.0	20 2 AAV74242	AAV74242 Cpg-N mot
11	20	100.0	20 2 AAX8536	AAZ8536 Cytosine-
12	20	100.0	20 2 AAZ28191	AAZ28191 Chlamydia
13	20	100.0	20 2 AAZ61012	AAZ61012 Nucleotid
14	20	100.0	20 3 AAZ48025	AAZ48025 Immune re
15	20	100.0	20 3 AAZ48022	AAZ48022 Immune re
16	20	100.0	20 3 AAZ47885	AAZ47885 Immunos
17	20	100.0	20 3 AAZ47887	AAZ47887 Immunos
18	20	100.0	20 3 AAZ50447	AAZ50447 Cpg adjuv
19	20	100.0	20 3 AAZ50447	AAZ50447 Cpg adjuv
20	20	100.0	20 3 AAZ59174	AAZ59174 Inflammat

21	20	100.0	20 3 AAZ93004	AAZ93004 Cpg motif
22	20	100.0	20 3 AAZ47601	AAZ47601 Murine im
23	20	100.0	20 3 AAC60277	AAC60277 Immunos
24	20	100.0	20 3 AAC64136	AAC64136 Immunos
25	20	100.0	20 4 AAH20390	AAH20390 Cpg motif
26	20	100.0	20 4 AAH20392	AAH20392 Cpg motif
27	20	100.0	20 4 AAH50580	AAH50580 Cpg motif
28	20	100.0	20 4 AAH19260	AAH19260 Cpg motif
29	20	100.0	20 4 AAF98805	AAF98805 Cpg immu
30	20	100.0	20 4 AAF59506	AAF59506 Immunos
31	20	100.0	20 4 AAF59501	AAF59501 Immunos
32	20	100.0	20 4 AAC82106	AAC82106 Oligonuc
33	20	100.0	20 4 AAF98748	AAF98748 Immunos
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## ALIGNMENTS

RESULT 1  
ID AAV60950 standard; DNA; 20 BP.  
XX AAV60950;  
AC  
XX  
DT 14-DEC-1998 (first entry)  
XX  
DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.  
XX  
KW ss; unmethylated Cpg dinucleotide; immune response; natural killer cell;  
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.  
XX  
OS Synthetic.  
XX  
PN W09840100-A1.  
XX  
PD 17-SEP-1998.  
XX  
PF 10-MAR-1998; 98WO-US004703.  
XX  
PR 10-MAR-1997; 97US-0040376P.  
XX  
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.  
PA (QIAG-) QIAGEN GMBH.  
PA (IOWA) UNIV IOWA RES FOUND.  
XX  
PI Davis HL, Schorr J, Krieg AM;  
XX WPI; 1998-520792/44.  
XX  
DR Use of oligonucleotides containing an unmethylated Cpg dinucleotide -  
XX useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen  
XX for inducing immune response in subject.  
XX  
PS Claim 14; Page 35; 67pp; English.  
XX  
CC Oligonucleotides containing at least 1 unmethylated Cpg dinucleotide  
CC affect the immune response in a subject by activating natural killer  
CC cells or redirecting a subject's immune response from a Th2 to a Th1  
CC response by inducing monocytic and other cells to produce Th1 cytokines.  
CC These nucleic acids containing at least 1 unmethylated Cpg can be used as  
CC an adjuvant, specifically to induce an immune response against an